Comparing the performance of BITFAM using TF-targets obtained from different databases
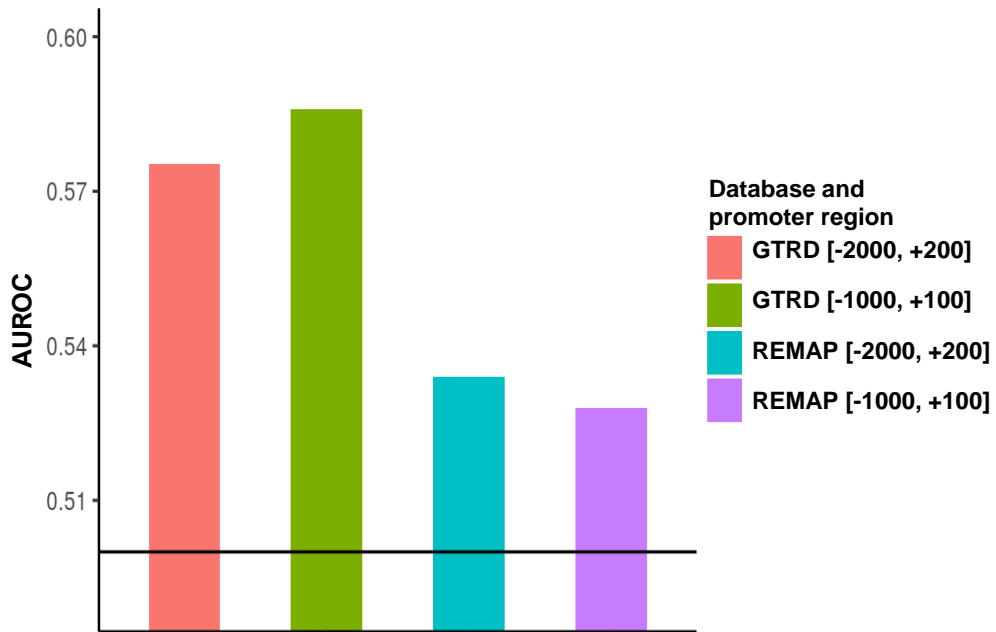
Figure S12. Comparison of distinct ChIP-seq input databases

Comparison of the performance of BITFAM using the default Gene Transcription Regulation Database (GTRD) ChIP-seq database versus the REMAP database. When applying BITFAM to the CRISPRi dataset, we found that using GTRD performed better than when using ReMAP (AUC 0.581 for GTRD on region [-1000, +100], AUC 0.575 for GTRD on region [-2000, +200], AUC 0.552 for ReMAP on region [-1000, +100], AUC 0.547 for ReMap on region [-2000, +200]).

Fig.S12